Applicant:
Warren and Swanson
Application No.: 09/389,537
Filed: September 2, 1999
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PATENT
DIVER1240-3

II. REMARKS

These remarks are in response to the Office Action mailed July 3, 2001. Applicants submit that the amendments to the claims are for clarity and should not be construed as amendments affecting patentability under *Festo Corp. v. Shoketsu Kinzoku Kogyo Kabushiki Co.*, 234 F.3d 558, 56 USPQ2d 1865 (Fed. Cir. 2000) (en banc). Additionally, new claims 28 and 29 have been added. As drafted, these claims are fully supported by the specification, as filed, and do not add new matter. Thus, upon entry of the amendment, claims 17-29 are under examination.

A. OBJECTION TO THE SPECIFICATION

The specification of the present application was objected to due to the following informalities, as set forth in Paper No. 12: the ATCC number, for example, on pages 3 and 6, is not specified, there is no description of Figures 9 and 10, the description of Figure 11 is incorrect, the specification incorporates expired provisional application 60/008,316 by reference, the specification does not contain sequence identifiers in all instances where the specification discusses sequences, and the paper copy and electronic copies of the Sequence Listing are different. As these objections have been remedied by the amendments of the present Response, it is respectfully requested that the above objections be withdrawn.

It is respectfully submitted that the reference to the ATCC number on pages 3 and 6 has been removed, as set forth above. As the language is no longer present in the specification, it is respectfully submitted that the objection is moot.

As the amendments set forth above provide accurate descriptions of Figures 9, 10 and 11, it is respectfully requested that the objection to these figures be withdrawn.

The specification is objected to in that expired provisional application 60/008,316 is incorporated by reference. It is respectfully submitted that an application was filed, claiming priority to provisional application 60/008,316 prior to expiration of the provisional application.

The amendment to the specification above has incorporated the serial number of the new U.S. Patent Number claiming priority to Provisional Application Serial Number 60/008,316. It is therefore respectfully submitted that this amendment remedies the incorporation of an expired application. As such, it is respectfully requested that the objection be withdrawn

The specification is also objected to, in that sequence identifiers are not used in all instances. It is respectfully submitted that the amendments to the specification, particularly those amendments made to the last two paragraphs on page 27, remedy the lack of sequence identifiers. It is therefore respectfully requested that the objection be withdrawn.

The application is also objected to in that the application fails to comply with the requirements for applications having nucleotide and/or amino acid sequences under 37 C.F.R. §§1.821-1.825. It is respectfully submitted that the Sequence Listing and computer readable form thereof were submitted in the above-referenced application by virtue of the "Permission to Use Sequence Listing" filed January 19, 2001. However, in response to the objection that the paper copy and electronic copies of the Sequence Listing are different, Applicants are submitting a substitute copy of the computer readable form of the sequence listing of the present application and a clean paper copy of the same. The substitute paper copy is identical to the substitute copy of the computer readable form and does not include new matter to the as-filed application. Submitted concurrently is an executed statement under 37 C.F.R. §1.825(b) to that effect. Accordingly, Applicants respectfully request entry of the substitute paper copy and the substitute copy of the computer readable form of the sequence listing. In view of the above, Applicants believe that the application now complies with the requirements for sequences under 37 C.F.R. §§1.821-1.825.

B. REJECTIONS UNDER 35 U.S.C.§112, FIRST PARAGRAPH

Applicants respectfully traverse the rejection of claims 17 to 27 under 35 U.S.C. § 112, first paragraph, for containing subject matter allegedly not described in the Specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors had possession

of the invention at the time of filing of the Application. In particular, it is alleged in Paper No. 12 that claims 17 to 27 are directed to a vast diverse class of enzymes with structural limitations, but no specific functional limitations. (Paper No. 12, page 4).

Applicants respectfully disagree. It is alleged in the Paper No. 12 that "[t]he claims are not drawn to an aspartate transaminase having an amino acid sequence that is 70% identical to SEQ ID NO:25 for example, but to any transaminase or aminotransferase." (Paper No. 12, page 8.) Applicants respectfully submit that the claims, as pending, include both structural and functional requirements for the claimed enzyme. Structurally, the claimed enzyme must be at least 70% identical to any one of SEQ ID NOS: 25-32. Functionally, the claimed enzyme must have transaminase or aminotransferase activity. If an enzyme does not possess both of these characteristics, it falls outside of the claim. The claims are not drawn to any transaminase or aminotransferase, as alleged in Paper No. 12, but to an enzyme that is at least 70% identical to any one of SEQ ID NOS: 25-32 and has transaminase or aminotransferase activity. As such, an enzyme of the claimed invention discloses sufficient identifying characteristics to allow one of skill in the art to distinguish a transaminase or aminotransferase of the invention from a transaminase or aminotransferase that does not fall within the scope of the claims. It is respectfully submitted that claims 17, 18 and claims dependent therefrom meet the written description requirement of 35 U.S.C. §112, first paragraph. Accordingly, the removal of the rejection is requested.

Additionally, the Examiner's attention is drawn to new claims 28 and 29 where claims 17 and 18, respectively, are further defined. Claims 28 and 29 specify that the enzyme claimed in claim 17 and used in the method of claim 18 have the same amino group acceptor and amino group donor as the enzyme to which it is at least 70% identical. Therefore the claims provide clarification of the structural and functional limitations of the enzyme in claims 17 and 18, in order to distinguish the claimed enzymes from all other enzymes or proteins.

Similarly, Applicants respectfully traverse the rejection of claims 17 to 27 under 35 U.S.C. § 112, first paragraph, for allegedly being non-enabled for a transaminase or aminotransferase having an amino acid sequence 70%, 80%, 90% or 95% identical to SEQ ID NOs: 25-32 and a method of use thereof.

Applicants respectfully draw the Examiner's attention to claims 17 and 18. As set forth above, these claims contain both structural and functional characteristics of the claimed enzyme. One of skill in the art would therefore be able to make and use the claimed invention without any undue burden. Even where there are multiple transaminase or aminotransferase activities, one of skill in the art would have known, at the time of filing of the application, how to determine whether an enzyme with at least 70% homology to any one of SEQ ID NOS: 25-32 has transaminase or aminotransferase activity or whether the enzyme does not have transaminase or aminotransferase activity. Therefore, claims 17, 18 and claims dependent therefrom meet the enablement requirement of 35 U.S.C. §112, first paragraph. Accordingly, the removal of the rejection is requested.

C. REJECTIONS UNDER 35 U.S.C. §112, SECOND PARAGRAPH

Applicants respectfully traverse the rejection of claims 17 to 27 under 35 U.S.C. § 112, second paragraph, as allegedly indefinite for failing to point out and distinctly claim the subject matter which Applicant regards as the invention. Applicants respectfully traverse the rejection.

Specifically, claims 17 and 18 are rejected for recitation of "the amino acid sequence set forth in SEQ ID NOs: 25-32." In accordance with the Examiner's suggestion, claims 17 and 18 have been amended to recite "any one of SEQ ID NOs: 25-32." As such, it is respectfully requested that the rejection be removed.

Similarly, claim 18 has been rejected for recitation of "an enzyme which is at least 70% identical to the amino acid sequence." In order to clarify the claim, the claim has been amended

to recite "an enzyme encoded by an amino acid sequence which is at least 70% identical to the amino acid sequence." As such, it is respectfully requested that the rejection be removed.

Claims 23 to 27 are rejected as confusing, as claims 23 to 27 refer to an enzyme of claim 18, where claim 18 is drawn to a method. The preamble of claims 23 to 27 has been amended to recite "The method of claim 18." As such, it is respectfully submitted that claims 23 to 27 are not confusing, as amended, and it is respectfully requested that the rejection be removed.

CONCLUSION

In summary, for the reasons set forth herein, Applicants maintain that claims 17 to 29 clearly and patentably define the invention, respectfully request that the Examiner reconsider the various grounds set forth in the Office Action, and respectfully request the allowance of the claims which are now pending.

If the Examiner would like to discuss any of the issues raised in the Office Action, Applicant's representative can be reached at (858) 677-1456. Please charge any additional fees, or make any credits, to Deposit Account No. 50-1355.

Respectfully submitted,

Lisa A. Haile

Date: December 3, 2001

Lisa A. Haile, J.D., Ph.D.
Reg. No. 38,347
Telephone: (858) 677-1456
Facsimile: (858) 677-1465

GRAY CARY WARE & FREIDENRICH LLP
4365 Executive Drive, Suite 1100
San Diego, California 92121-2133
USPTO Cust mer Number 28213

Gray Cary\GT\6254523.3
104703-158406

Applicant:
Warren and Swanson
Application No.: 09/389,537
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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

On page 3:

In accordance with another aspect of the present invention there are provided isolated nucleic acid molecules encoding mature polypeptides expressed by the DNA [contained in ATCC Deposit No. _______] encoding an enzyme of the present invention.

On page 5:

[Figure 9 is a diagrammatic illustration of the assay used to assess aminotransferase activity of the proteins using glutamate dehydrogenase.] Figure 9 shows the full-length DNA (SEQ ID NO.: 35) and corresponding deduced amino acid sequence (SEQ ID NO.: 36) of *Ammonifex degensii* histidinol phosphate aminotransferase.

Figure 10 shows the full-length DNA (SEQ ID NO.: 39) and corresponding deduced amino acid sequence (SEQ ID NO.: 40) of *Aquifex* aspartate aminotransferase.

Figure 11 is a diagram of the assay used to assess aminotransferase activity of the proteins using glutamate dehydrogenase.

On page 6:

In accordance with another aspect of the present invention, there are provided isolated polynucleotides encoding the enzymes of the present invention. The deposited material is a mixture of genomic clones comprising DNA encoding an enzyme of the present invention. Each genomic clone comprising the respective DNA has been inserted into a pQE vector (Quiagen, Inc., Chatsworth, CA). [The deposit has been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, USA, on December 13, 1995 and assigned ATCC Deposit No. __________.]

On page 22:

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Transaminases are highly stereoselective, and most use L-amino acids as substrates. Using the approach disclosed in [a] commonly assigned issued U.S. Patent Number 5,939,250 [co-pending provisional application Serial No. 60/008,316, filed on December 7, 1995], filed on December 7, 1996 and entitled "Combinatorial Enzyme Development," the disclosure of which is incorporated herein by reference in its entirety, one can convert the transaminases of the invention to use D-amino acids as substrates. Such conversion makes possible a broader array of transaminase applications. For instance, D-valine can be used in the manufacture of synthetic pyrethroids. D-phenylglycine and its derivatives can be useful as components of β-lactam antibiotics. Further the thermostable transaminases have superior stability at higher temperatures and in organic solvents. Thus, they are better suited to utilize either L- and/or D-maino acids for production of optically pure chiral compounds used in pharmaceutical, agricultural, and other chemical manfactures.

On page 27:
Ammonifex degensii hp aminotransferase
5'-CCGAGAATTCATTAAAGAGGAGAAATTAACTATGGCAGTCAAAGTGCGGCCT (SEQ ID NO: 33)
3'-CGGAGGATCCTTATCCAAAGCTTCCAGGAAG (SEQ ID NO: 34)
Homology information:
Closest to *Bacillus subtilis* (reference: Henner, D.J., Band., Flaggs G., Chen E.; Gene 49:147-152(1886). Percent similarity:65.084 Percent Identity 44.134

On page 27:
Aquifex aspartate aminotransferase
5'-CCGAGAATTCATTAAAGAGGAGAAATTAACTATGAGAAAAGGACTTGCAAGT (SEQ ID NO: 37)
3'-CGGAGGATCCTTAGATCTCTTCAAGGGCTTT (SEQ ID NO: 38)

Closest to *Bacillus subtilis* (Sorkin, A.V., Azevedo, V., Zumstein, E., Galleron, N., Ehrlich, S.D. and Serror, P. Determination and analysis of the nucleotide sequence of the Bacillus subtilis chromosome region between serA and kdg loci cloned in yeast artificial chromosome Unpublished (1995). Percent similarity: 71.611 Percent identity: 52.685

<u>In the claims:</u>

17. (Amended) An isolated enzyme [comprising a member selected from the group consisting of an enzyme] comprising an amino acid sequence which is at least 70% identical to [the amino acid sequence set forth in] <u>any one of</u> SEQ ID NOS:25-32 when aligned using the BLASTN program of the National Center for Biotechnology Information, wherein the enzyme has [activity as a] transaminase or aminotransferase <u>activity</u>.

18. (Amended) A method for transferring an amino group from an amino acid to an α-keto acid comprising:

contacting an amino acid in the presence of an α-keto acid with an isolated enzyme selected from the group consisting of an enzyme <u>encoded by an amino acid sequence</u> which is at least 70% identical to [the amino acid sequence set forth in] <u>any one of</u> SEQ ID NOs: 25-32 when aligned using the BLASTN program of the National Center for Biotechnology Information <u>wherein the enzyme has transaminase or aminotransferase activity;</u> and

thereby transferring an amino group from the amino acid to the α-keto acid.

19. (Amended) An enzyme of claim 17, wherein the amino acid sequence <u>of the isolated enzyme</u> is at least 80% identical.

20. (Amended) An enzyme of claim 17, wherein the amino acid sequence <u>of the isolated enzyme</u> is at least 90% identical.

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21. (Amended) An enzyme of claim 17, wherein the amino acid sequence of the isolated enzyme is at least 95% identical.

22. (Amended) An enzyme of claim 21, wherein the isolated enzyme is microbial.

23. (Amended) [An enzyme] The method of claim 18, wherein the amino acid sequence of the isolated enzyme is at least 80% identical.

24. (Amended) [An enzyme] The method of claim 18, wherein the amino acid sequence of the isolated enzyme is at least 90% identical.

25. (Amended) [An enzyme] The method of claim 18, wherein the amino acid sequence of the isolated enzyme is at least 95% identical.

26. (Amended) [An enzyme] The method of claim 25, wherein the isolated enzyme is microbial.

27. (Amended) [An enzyme] The method of claim 25, wherein the isolated enzyme converts about 400 μmoles of α-keto acid per minute per mg of the enzyme.

Attorney Docket No.: DIVER1240-3

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Warren and Swanson	Art Unit:	1652
Serial No.:	09/389,537	Examiner:	Slobodyansky E.
Filed:	September 2, 1999		
Title:	TRANSAMINASES AND AMINOTRANSFERASES		

Commissioner for Patents
Washington, D.C. 20231

VERIFIED STATEMENT UNDER 37 C.F.R. § 1.821(f)

Sir:

I, Mikhail Bayley, declare that I personally prepared the paper and the computer-readable copies of the Sequence Listing filed herewith in the above-entitled case and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 11/30/2001

Mikhail Bayley

Mikhail Bayley

GRAY CARY WARE & FREIDENRICH LLP
4365 Executive Drive, Suite 1100
San Diego, CA 92121-2133

Customer Number: 28213

CERTIFICATION UNDER 37 CFR §1.8	
I hereby certify that the documents referred to as enclosed herein are being deposited with the United States Postal Service as first class mail on this date, December 3, 2001, in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231.	
Aldon Griffis	
Name of Person Mailing Paper	
Aldon Griffis	
Signature	December 3, 2001 Date

Gray Cary\GT\6259349.1
104703-158406

Attorney Docket No.: DIVER1240-3

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Warren and Swanson	Art Unit:	1652
Serial No.:	09/389,537	Examiner:	Slobodyansky E.
Filed:	September 2, 1999		
Title:	TRANSAMINASES AND AMINOTRANSFERASES		

Commissioner for Patents
Washington, D.C. 20231

STATEMENT UNDER 37 C.F.R. §§ 1.821(f) and (g)

Sir:

I hereby state, as required by 37 C.F.R. § 1.821(f), that the information recorded in computer readable form is identical to the written sequence listing.

I hereby state that the submission, filed in accordance with 37 C.F.R. § 1.821 (g), herein does not include new matter.

Respectfully submitted,

Date: December 3, 2001

Lisa A. Haile, J.D., Ph.D.
Reg. No. 38,347
Telephone: (858) 677-1456
Facsimile: (858) 677-1465

GRAY CARY WARE & FREIDENRICH LLP
4365 Executive Drive, Suite 1100
San Diego, CA 92121-2133

Customer Number: 28213

CERTIFICATION UNDER 37 CFR §1.8	
I hereby certify that the documents referred to as enclosed herein are being deposited with the United States Postal Service as first class mail on this date, December 3, 2001, in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231.	
Aldon Griffis	
Name of Person Mailing Paper	
	December 3, 2001
Signature	Date

Gray Cary\GT\6259361.1
104703-158406

SEQUENCE LISTING

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SWANSON, Ronald

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ggaatagagc tggtgaagga caaagaaaag ggagaacctt tcccttacgg tgaaaggacg 1200

ggatttaagg tggcttacaa gtgcagggaa aaaggggtgt tttgagacc gctcggagac 1260

gttatggtat tgatgatgcc tcttgtaata gaggaagacg aaatgaacta cgttattgat 1320

acacttaaat gggcaattaa agagcttgaa aaagaggtgt ag 1362

<210> 20
<211> 1032
<212> DNA
<213> Aquifex

<400> 20
atgacatact taatgaacaa ttacgcaagg ttgcccgtaa agtttgtaag gggaaaaggt 60

gtttacctgt acgatgagga aggaaaggag tatcttgact ttgtctccgg tataggcgtc 120

aactccctcg gtcacgctta cccaaaactc acagaagctc taaaagaaca ggttgagaaa 180

ctcctccacg tttcaaatct ttacgaaaac ccgtggcagg aagaactggc tcacaaactt 240

gtaaaacact tctggacaga agggaaggta tttttcgcaa acagcggaac ggaaagtgta 300

gaggcggcta taaagctcgc aaggaagtac tggagggata aaggaaagaa caagtggaag 360

tttatatcct ttgaaaactc tttccacggg agaacctacg gtagcctctc cgcaacggga 420

cagccaaagt tccacaaagg ctttgaacct ctagttcctg gattttctta cgcaaagctg 480

aacgatatag acagcgttta caaactccta gacgaggaaa ccgcggggat aattattgaa 540

gttatacaag gagagggcgg agtaaacgag gcgagtgagg attttctaag taaactccag 600

gaaatttgta aagaaaaaga tgtgctctta attatagacg aagtgcaaac gggaatagga 660

aggaccgggg aattctacgc atatcaacac ttcaatctaa aaccggacgt aattgcgctt 720

gcgaagggac tcggaggagg tgtgccaata ggtgccatcc ttgcaaggga agaagtggcc 780

cagagcttta ctcccggctc ccacggctct accttcggag gaaacccctt agcctgcagg 840

gcgggaacag tggtagtaga tgaagttgaa aaactcctgc ctcacgtaag ggaagtgggg 900

aattacttca aagaaaaact gaaggaactc ggcaaaggaa aggtaaaggg aagaggattg 960

atgctcggtc ttgaacttga aagagagtgt aaagattacg ttctcaaggc tcttgaaagg 1020

gacttctcat aa 1032

<210> 21
<211> 1197
<212> DNA
<213> Ammonifex degensii

<400> 21
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accaaggcca aggagctttt gcggcagggg gaaagggtca tcaatttcgg ggcgggggag 120

ccggacttcg atacaccgga acacatcaag gaagcggcga agcgagcttt agatcagggc 180

ttcaccaagt acacgccggt ggctgggatc ttacctcttc gggaggccat atgcgagaag 240

ctttaccgcg acaatcaact ggaatacagc ccgaatgaga tcgtggtctc ctgtggcgcc 300

aagcattcta ttttcaacgc tctgcaggtc ctcctggacc cgggggacga ggtgataatc 360

cccgtcccct actggacttc ctatccggag caggtgaagc tggcgggagg ggtgccggtt 420

ttcgtcccca cctctcccga gaacgacttc aagctcaggc cggaagatct acgtgcggct 480

gtaaccccgc gcacccgcct tttgatcctc aattcccggg ccaaccccac aggcaccgtt 540

taccgccggg aggaacttat cggcttagcg gaggtagccc tggaggccga cctatggatc 600

ttgtcggacg agatctacga aaagctgatc tacgacggga tggagcacgt gagcatagcc 660

gcgctcgacc cggaggtcaa aaagcgcacg attgtggtaa acggtgtttc caaggcttac 720

gccatgaccg gttggcgcat aggttatgct gccgctcccc ggccgatagc ccaggccatg 780

accaacctcc aaagccacag tacctctaac cccacttccg tagcccaggc ggcggcgctg 840

gccgctctga aggggccaca agagccggtg gagaacatgc gccgggcttt tcaaaagcgg 900

cgggatttca tctggcagta cctaaactcc ttacccggag tgcgctgccc caaacccttta 960

ggggcctttt acgtctttcc agaagttgag cgggcttttg ggccgccgtc taaaaggacg 1020

ggaaatacta ccgctagcga cctggccctt ttcctcctgg aagagataaa agtggccacc 1080

gtggctgggg ctgcctttgg ggacgatcgc tacctgcgct tttcctacgc cctgcggctg 1140

gaagatatcg aagaggggat gcaacggttt aaagaattga tcgaagcggc actttaa 1197

<210> 22
<211> 1779
<212> DNA
<213> Aquifex

<400> 22
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cttgagagac tcgaatacag ggttacgac tccgcgggag ttgcccttat agaagacggg 120

aaactcatag ttgaaaagaa gaagggaaag ataagggaac tcgttaaagc gctatgggga 180

aaggattaca aggctaaaac gggtataggt cacacacgct gggcaaccca cggaaagccc 240

acggacgaga acgcccaccc ccacaccgac gaaaaaggtg agtttgcagt agttcacaac 300

gggataatag aaaactactt agaactaaaa gaggaactaa agaaggaagg tgtaaagttc 360

aggtccgaaa cagacacaga agttatagcc cacctcatag cgaagaacta caggggggac 420

ttactggagg ccgttttaaa aaccgtaaag aaattaaagg gtgcttttgc ctttgcggtt 480

ataacggttc acgaaccaaa cagactaata ggagtgaagc aggggagtcc tttaatcgtc 540

ggactcggag aaggagaaaa cttcctcgct tcagatattc ccgcaatact tccttacacg 600

aaaaagatta ttgttcttga tgacggggaa atagcggacc tgactcccga cactgtgaac 660

atttacaact ttgagggaga gcccgtttca aaggaagtaa tgattacgcc ctgggatctt 720

gtttctgcgg aaaagggtgg ttttaaacac ttcatgctaa aagagatata cgaacagccc 780

aaagccataa acgacacact caagggtttc ctctcaaccg aagacgcaat acccttttaag 840

ttaaaagact tcagaagggt tttaataata gcgtgcggga cctcttacca cgcgggcttc 900

gtcggaaagt actggataga gagatttgca ggtgttccca cagaggtaat ttacgcttcg 960

gaattcaggt atgcggacgt tcccgtttcg gacaaggata tcgttatcgg aatttcccag 1020

tcaggagaga ccgctgacac aaagtttgcc cttcagtccg caaaggaaaa gggagccttt 1080

accgtgggac tcgtaaacgt agtgggaagt gccatagaca gggagtcgga cttttccctt 1140

cacacacatg cgggacccga aataggcgtg gcggctacaa agaccttcac cgcacagttc 1200

accgcactct acgccctttc ggtaagggaa agtgaggaga gggaaaatct aataagactc 1260

cttgaaaagg ttccatcact cgttgaacaa acactgaaca ccgcagaaga agtggagaag 1320

gtagcggaaa agtacatgaa aaagaaaaac atgctttacc tcggaaggta cttaaattac 1380

cccatagcgc tggagggagc tcttaaactt aaagaaattt cttacataca cgcggaaggt 1440

tatcccgcag gggagatgaa gcacggtccc atagccctca tagacgaaaa catgccggtt 1500

gtggtaatcg caccgaaaga cagggtttac gagaagatac tctcaaacgt agaagaggtt 1560

ctcgcaagaa agggaagggt tatttctgta ggctttaaag gagacgaaac tctcaaaagc 1620

aaatccgaga gcgttatgga aatcccgaag gcagaagaac cgataactcc tttcttgacg 1680

gtaatacccc tgcaactctt tgcctacttt atagcgagca aactgggact ggatgtggat 1740

cagccgagaa atctcgccaa aacggtcacg gtggaataa 1779

<210> 23
<211> 1065
<212> DNA
<213> Aquifex

<400> 23
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gtcaggcttt cctctaacga attcccctac gactttcccg aggagataaa acaaagggcc 120

ttagaagaat taaaaaaggt tcccttgaac aaatacccag accccgaagc gaaagagtta 180

aaagcggttc ttgcggattt tttcggcgtt aaggaagaaa atttagttct cggtaacggt 240

tcggacgaac tcatatacta cctctcaata gctataggtg aactttacat accccgtttac 300

atacctgttc ccacctttcc catgtacgag ataagtgcga aagttctcgg aagacccctc 360

gtaaaggttc aactggacga aaactttgat atagacttag aaagaagtat tgaattaata 420

gagaaagaaa aacccgttct cgggtacttt gcttacccaa acaaccccac gggaaacctc 480

ttttccaggg gaaagattga ggagataaga aacaggggtg ttttctgtgt aatagacgaa 540

gcctactatc attactccgg agaaaccttt ctggaagacg cgctcaaaag ggaagatacg 600

gtagttttga ggacactttc aaaaatcggt atggcgagtt taagggtagg gattttaata 660

gggaaggggg aaatcgtctc agaaattaac aaggtgagac tccccttcaa cgtgacctac 720

ccctctcagg tgatggcaaa agttctcctc acggagggaa gagaattcct aatggaaaag 780

atacaggagg ttgtaacaga gcgagaaagg atgtacgacg aaatgaagaa aatagaagga 840

gttgaggttt ttccgagtaa ggctaacttc ttgcttttca gaacgcctta ccccgcccac 900

gaggtttatc aggagctact gaaaagggat gtcctcgtca ggaacgtatc ttacatggaa 960

ggactccaaa agtgcctcag ggtaagcgta gggaaaccgg aagaaaacaa caagtttctg 1020

gaagcactgg aggagagtat aaaatccctt tcaagctctc tttaa 1065

<210> 24
<211> 912
<212> DNA
<213> Pyrobaculum aerophilum

<400> 24
atgaagccgt acgctaaata tatctggctt gacggcagaa tacttaagtg ggaagacgcg 60

aaaatacacg tgttgactca cgcgcttcac tacggaacct ctatattcga gggaataaga 120

gggtattgga acggcgataa tttgctcgtc tttaggttag aagaacacat cgaccgcatg 180

tacagatcgg ctaagatact aggcataaat attccgtata caagagagga agtccgccaa 240

gctgtactag agaccataaa ggctaataac ttccgagagg atgtctacat aagacctgtg 300

gcgtttgtcg cctcgcagac ggtgacgctt gacataagaa atttggaagt ctccctcgcg 360

gttattgtat tcccatttgg caaatacctc tcgcccaacg gcattaaggc aacgattgta 420

agctggcgta gagtacataa tacaatgctc cctgtgatgg caaaaatcgg cggtatatat 480

gtaaactctg tacttgcgct tgtagaggct agaagcaggg gatttgacga ggctttatta 540

atggacgtta acggttatgt tgttgagggt tctggagaga atattttcat tgtcagaggt 600

ggaaggcttt tcacgccgcc agtacacgaa tctatcctcg agggaattac gagggatacg 660

gtaataaagc tcagcgggga tgtgggactt cgggtggagg aaaagcctat tacgagggag 720

gaggtgtata cagccgacga ggtgtttttta gtaggaaccg ccgcagagat aacgccagtg 780

gtggaggttg acggcagaac aatcggcaca ggcaagccgg gccccattac gacaaaaata 840

gctgagctgt actcaaacgt cgtgagaggc aaagtagaga aatacttaaa ttggatcact 900

cctgtgtatt ag 912

<210> 25
<211> 414
<212> PRT
<213> Aquifex

<400> 25

Met Ile Glu Asp Pro M t Asp Trp Ala Phe Pro Arg Ile Lys Arg Leu
1 5 10 15

Pro Gln Tyr Val Phe Ser Leu Val Asn Glu Leu Lys Tyr Lys Leu Arg
20 25 30

Arg Glu Gly Glu Asp Val Val Asp Leu Gly Met Gly Asn Pro Asn Met
35 40 45

Pro Pro Ala Lys His Ile Ile Asp Lys Leu Cys Glu Val Ala Gln Lys
50 55 60

Pro Asn Val His Gly Tyr Ser Ala Ser Arg Gly Ile Pro Arg Leu Arg
65 70 75 80

Lys Ala Ile Cys Asn Phe Tyr Glu Glu Arg Tyr Gly Val Lys Leu Asp
85 90 95

Pro Glu Arg Glu Ala Ile Leu Thr Ile Gly Ala Lys Glu Gly Tyr Ser
100 105 110

His Leu Met Leu Ala Met Ile Ser Pro Gly Asp Thr Val Ile Val Pro
115 120 125

Asn Pro Thr Tyr Pro Ile His Tyr Tyr Ala Pro Ile Ile Ala Gly Gly
130 135 140

Glu Val His Ser Ile Pro Leu Asn Phe Ser Asp Asp Gln Asp His Gln
145 150 155 160

Glu Glu Phe Leu Arg Arg Leu Tyr Glu Ile Val Lys Thr Ala Met Pro
165 170 175

Lys Pro Lys Ala Val Val Ile Ser Phe Pro His Asn Pro Thr Thr Ile
180 185 190

Thr Val Glu Lys Asp Phe Phe Lys Glu Ile Val Lys Phe Ala Lys Glu
195 200 205

His Gly Leu Trp Ile Ile His Asp Phe Ala Tyr Ala Asp Ile Ala Phe
210 215 220

Asp Gly Tyr Lys Pro Pro Ser Ile Leu Glu Ile Glu Gly Ala Lys Asp
225 230 235 240

Val Ala Val Glu Leu Tyr Ser Met Ser Lys Gly Phe Ser Met Ala Gly
245 250 255

Trp Arg Val Ala Phe Val Val Gly Asn Glu Ile Leu Ile Lys Asn Leu
260 265 270

Ala His Leu Lys Ser Tyr Leu Asp Tyr Gly Ile Phe Thr Pro Ile Gln
275 280 285

Val Ala Ser Ile Ile Ala Leu Glu Ser Pro Tyr Glu Ile Val Glu Lys
290 295 300

Thr Ala Lys Val Tyr Gln Lys Arg Arg Asp Val Leu Val Glu Gly Leu
305 310 315 320

Asn Arg Leu Gly Trp Lys Val Lys Lys Pro Lys Ala Thr Met Phe Val
325 330 335

Trp Ala Lys Ile Pro Glu Trp Ile Asn Met Asn Ser Leu Asp Phe Ser

340 345 350

Leu Phe Leu Leu Lys Glu Ala Lys Val Ala Val Ser Pr Gly Val Gly
355 360 365

Phe Gly Gln Tyr Gly Glu Gly Tyr Val Arg Phe Ala Leu Val Glu Asn
370 375 380

Glu His Arg Ile Arg Gln Ala Ile Arg Gly Ile Arg Lys Ala Phe Arg
385 390 395 400

Lys Leu Gln Lys Glu Arg Lys Leu Glu Pro Glu Arg Ser Ala
405 410

<210> 26
<211> 373
<212> PRT
<213> Aquifex

<400> 26

Met Asp Arg Leu Glu Lys Val Ser Pro Phe Ile Val Met Asp Ile Leu
1 5 10 15

Ala Gln Ala Gln Lys Tyr Glu Asp Val Val His Met Glu Ile Gly Glu
20 25 30

Pro Asp Leu Glu Pro Ser Pro Lys Val Met Glu Ala Leu Glu Arg Ala
35 40 45

Val Lys Glu Lys Thr Phe Phe Tyr Thr Pro Ala Leu Gly Leu Trp Glu
50 55 60

Leu Arg Glu Arg Ile Ser Glu Phe Tyr Arg Lys Lys Tyr Ser Val Glu
65 70 75 80

Val Ser Pro Glu Arg Val Ile Val Thr Thr Gly Thr Ser Gly Ala Phe
85 90 95

Leu Val Ala Tyr Ala Val Thr Leu Asn Ala Gly Glu Lys Ile Ile Leu
100 105 110

Pro Asp Pro Ser Tyr Pro Cys Tyr Lys Asn Phe Ala Tyr Leu Leu Asp
115 120 125

Ala Gln Pro Val Phe Val Asn Val Asp Lys Glu Thr Asn Tyr Glu Val
130 135 140

Arg Lys Glu Met Ile Glu Asp Ile Asp Ala Lys Ala Leu His Ile Ser
145 150 155 160

Ser Pro Gln Asn Pro Thr Gly Thr Leu Tyr Ser Pro Glu Thr Leu Lys
165 170 175

Glu Leu Ala Glu Tyr Cys Glu Glu Lys Gly Met Tyr Phe Ile Ser Asp
180 185 190

Glu Ile Tyr His Gly Leu Val Tyr Glu Gly Arg Glu His Thr Ala Leu
195 200 205

Glu Phe Ser Asp Arg Ala Ile Val Ile Asn Gly Phe Ser Lys Tyr Phe

210 215 220

Cys Met Pro Gly Phe Arg Ile Gly Trp Met Ile Val Pr Glu Glu Leu
225 230 235 240

Val Arg Lys Ala Glu Ile Val Ile Gln Asn Val Phe Ile Ser Ala Pro
245 250 255

Thr Leu Ser Gln Tyr Ala Ala Leu Glu Ala Phe Asp Tyr Glu Tyr Leu
260 265 270

Glu Lys Val Arg Lys Thr Phe Glu Glu Arg Arg Asn Phe Leu Tyr Gly
275 280 285

Glu Leu Lys Lys Leu Phe Lys Ile Asp Ala Lys Pro Gln Gly Ala Phe
290 295 300

Tyr Val Trp Ala Asn Ile Ser Asp Tyr Ser Thr Asp Ser Tyr Glu Phe
305 310 315 320

Ala Leu Lys Leu Leu Arg Glu Ala Arg Val Ala Val Thr Pro Gly Val
325 330 335

Asp Phe Gly Lys Asn Lys Thr Lys Glu Tyr Ile Arg Phe Ala Tyr Thr
340 345 350

Arg Lys Ile Glu Glu Leu Lys Glu Gly Val Glu Arg Ile Lys Lys Phe
355 360 365

Leu Glu Lys Leu Ser
370

<210> 27
<211> 453
<212> PRT
<213> Aquifex

<400> 27

Met Trp Glu Leu Asp Pro Lys Thr Leu Glu Lys Trp Asp Lys Glu Tyr
1 5 10 15

Phe Trp His Pro Phe Thr Gln Met Lys Val Tyr Arg Glu Glu Glu Asn
20 25 30

Leu Ile Phe Glu Arg Gly Glu Gly Val Tyr Leu Trp Asp Ile Tyr Gly
35 40 45

Arg Lys Tyr Ile Asp Ala Ile Ser Ser Leu Trp Cys Asn Val His Gly
50 55 60

His Asn His Pro Lys Leu Asn Asn Ala Val Met Lys Gln Leu Cys Lys
65 70 75 80

Val Ala His Thr Thr Thr Leu Gly Ser Ser Asn Val Pro Ala Ile Leu
85 90 95

Leu Ala Lys Lys Leu Val Glu Ile Ser Pro Glu Gly Leu Asn Lys Val
100 105 110

Phe Tyr Ser Glu Asp Gly Ala Glu Ala Val Glu Ile Ala Ile Lys Met

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        115                 120                 125

Ala Tyr His Tyr Trp Lys Asn Lys Gly Val Lys Gly Lys Asn Val Phe
    130                 135                 140

Ile Thr Leu Ser Glu Ala Tyr His Gly Asp Thr Val Gly Ala Val Ser
145                 150                 155                 160

Val Gly Gly Ile Glu Leu Phe His Gly Thr Tyr Lys Asp Leu Leu Phe
                165                 170                 175

Lys Thr Ile Lys Leu Pro Ser Pro Tyr Leu Tyr Cys Lys Glu Lys Tyr
            180                 185                 190

Gly Glu Leu Cys Pro Glu Cys Thr Ala Asp Leu Leu Lys Gln Leu Glu
        195                 200                 205

Asp Ile Leu Lys Ser Arg Glu Asp Ile Val Ala Val Ile Met Glu Ala
    210                 215                 220

Gly Ile Gln Ala Ala Ala Gly Met Leu Pro Phe Pro Pro Gly Phe Leu
225                 230                 235                 240

Lys Gly Val Arg Glu Leu Thr Lys Lys Tyr Asp Thr Leu Met Ile Val
                245                 250                 255

Asp Glu Val Ala Thr Gly Phe Gly Arg Thr Gly Thr Met Phe Tyr Cys
            260                 265                 270

Glu Gln Glu Gly Val Ser Pro Asp Phe Met Cys Leu Gly Lys Gly Ile
        275                 280                 285

Thr Gly Gly Tyr Leu Pro Leu Ala Ala Thr Leu Thr Thr Asp Glu Val
    290                 295                 300

Phe Asn Ala Phe Leu Gly Glu Phe Gly Glu Ala Lys His Phe Tyr His
305                 310                 315                 320

Gly His Thr Tyr Thr Gly Asn Asn Leu Ala Cys Ser Val Ala Leu Ala
                325                 330                 335

Asn Leu Glu Val Phe Glu Glu Glu Arg Thr Leu Glu Lys Leu Gln Pro
            340                 345                 350

Lys Ile Lys Leu Leu Lys Glu Arg Leu Gln Glu Phe Trp Glu Leu Lys
        355                 360                 365

His Val Gly Asp Val Arg Gln Leu Gly Phe Met Ala Gly Ile Glu Leu
    370                 375                 380

Val Lys Asp Lys Glu Lys Gly Glu Pro Phe Pro Tyr Gly Glu Arg Thr
385                 390                 395                 400

Gly Phe Lys Val Ala Tyr Lys Cys Arg Glu Lys Gly Val Phe Leu Arg
                405                 410                 415

Pro Leu Gly Asp Val Met Val Leu Met Met Pro Leu Val Ile Glu Glu
            420                 425                 430

Asp Glu Met Asn Tyr Val Ile Asp Thr Leu Lys Trp Ala Ile Lys Glu
        435                 440                 445
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Leu Glu Lys Glu Val
450

<210> 28
<211> 343
<212> PRT
<213> Aquifex

<400> 28

Met Thr Tyr Leu Met Asn Asn Tyr Ala Arg Leu Pro Val Lys Phe Val
1 5 10 15

Arg Gly Lys Gly Val Tyr Leu Tyr Asp Glu Glu Gly Lys Glu Tyr Leu
20 25 30

Asp Phe Val Ser Gly Ile Gly Val Asn Ser Leu Gly His Ala Tyr Pro
35 40 45

Lys Leu Thr Glu Ala Leu Lys Glu Gln Val Glu Lys Leu Leu His Val
50 55 60

Ser Asn Leu Tyr Glu Asn Pro Trp Gln Glu Glu Leu Ala His Lys Leu
65 70 75 80

Val Lys His Phe Trp Thr Glu Gly Lys Val Phe Phe Ala Asn Ser Gly
85 90 95

Thr Glu Ser Val Glu Ala Ala Ile Lys Leu Ala Arg Lys Tyr Trp Arg
100 105 110

Asp Lys Gly Lys Asn Lys Trp Lys Phe Ile Ser Phe Glu Asn Ser Phe
115 120 125

His Gly Arg Thr Tyr Gly Ser Leu Ser Ala Thr Gly Gln Pro Lys Phe
130 135 140

His Lys Gly Phe Glu Pro Leu Val Pro Gly Phe Ser Tyr Ala Lys Leu
145 150 155 160

Asn Asp Ile Asp Ser Val Tyr Lys Leu Leu Asp Glu Glu Thr Ala Gly
165 170 175

Ile Ile Ile Glu Val Ile Gln Gly Glu Gly Gly Val Asn Glu Ala Ser
180 185 190

Glu Asp Phe Leu Ser Lys Leu Gln Glu Ile Cys Lys Glu Lys Asp Val
195 200 205

Leu Leu Ile Ile Asp Glu Val Gln Thr Gly Ile Gly Arg Thr Gly Glu
210 215 220

Phe Tyr Ala Tyr Gln His Phe Asn Leu Lys Pro Asp Val Ile Ala Leu
225 230 235 240

Ala Lys Gly Leu Gly Gly Gly Val Pro Ile Gly Ala Ile Leu Ala Arg
245 250 255

Glu Glu Val Ala Gln Ser Phe Thr Pro Gly Ser His Gly Ser Thr Phe
260 265 270

Gly Gly Asn Pro Leu Ala Cys Arg Ala Gly Thr Val Val Val Asp Glu
275 280 285

Val Glu Lys Leu Leu Pro His Val Arg Glu Val Gly Asn Tyr Phe Lys
290 295 300

Glu Lys Leu Lys Glu Leu Gly Lys Gly Lys Val Lys Gly Arg Gly Leu
305 310 315 320

Met Leu Gly Leu Glu Leu Glu Arg Glu Cys Lys Asp Tyr Val Leu Lys
325 330 335

Ala Leu Glu Arg Asp Phe Ser
340

<210> 29
<211> 398
<212> PRT
<213> Ammonifex degensii

<400> 29

Met Arg Lys Leu Ala Glu Arg Ala Gln Lys Leu Ser Pro Ser Pro Thr
1 5 10 15

Leu Ser Val Asp Thr Lys Ala Lys Glu Leu Leu Arg Gln Gly Glu Arg
20 25 30

Val Ile Asn Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Glu His
35 40 45

Ile Lys Glu Ala Ala Lys Arg Ala Leu Asp Gln Gly Phe Thr Lys Tyr
50 55 60

Thr Pro Val Ala Gly Ile Leu Pro Leu Arg Glu Ala Ile Cys Glu Lys
65 70 75 80

Leu Tyr Arg Asp Asn Gln Leu Glu Tyr Ser Pro Asn Glu Ile Val Val
85 90 95

Ser Cys Gly Ala Lys His Ser Ile Phe Asn Ala Leu Gln Val Leu Leu
100 105 110

Asp Pro Gly Asp Glu Val Ile Ile Pro Val Pro Tyr Trp Thr Ser Tyr
115 120 125

Pro Glu Gln Val Lys Leu Ala Gly Gly Val Pro Val Phe Val Pro Thr
130 135 140

Ser Pro Glu Asn Asp Phe Lys Leu Arg Pro Glu Asp Leu Arg Ala Ala
145 150 155 160

Val Thr Pro Arg Thr Arg Leu Leu Ile Leu Asn Ser Pro Ala Asn Pro
165 170 175

Thr Gly Thr Val Tyr Arg Arg Glu Glu Leu Ile Gly Leu Ala Glu Val
180 185 190

Ala Leu Glu Ala Asp Leu Trp Ile Leu Ser Asp Glu Ile Tyr Glu Lys
195 200 205

Leu Il Tyr Asp Gly Met Glu His Val Ser Ile Ala Ala Leu Asp Pro
210 215 220

Glu Val Lys Lys Arg Thr Ile Val Val Asn Gly Val Ser Lys Ala Tyr
225 230 235 240

Ala Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Ala Pro Arg Pro Ile
245 250 255

Ala Gln Ala Met Thr Asn Leu Gln Ser His Ser Thr Ser Asn Pro Thr
260 265 270

Ser Val Ala Gln Ala Ala Ala Leu Ala Ala Leu Lys Gly Pro Gln Glu
275 280 285

Pro Val Glu Asn Met Arg Arg Ala Phe Gln Lys Arg Arg Asp Phe Ile
290 295 300

Trp Gln Tyr Leu Asn Ser Leu Pro Gly Val Arg Cys Pro Lys Pro Leu
305 310 315 320

Gly Ala Phe Tyr Val Phe Pro Glu Val Glu Arg Ala Phe Gly Pro Pro
325 330 335

Ser Lys Arg Thr Gly Asn Thr Thr Ala Ser Asp Leu Ala Leu Phe Leu
340 345 350

Leu Glu Glu Ile Lys Val Ala Thr Val Ala Gly Ala Ala Phe Gly Asp
355 360 365

Asp Arg Tyr Leu Arg Phe Ser Tyr Ala Leu Arg Leu Glu Asp Ile Glu
370 375 380

Glu Gly Met Gln Arg Phe Lys Glu Leu Ile Glu Ala Ala Leu
385 390 395

<210> 30
<211> 592
<212> PRT
<213> Aquifex

<400> 30

Met Cys Gly Ile Val Gly Tyr Val Gly Arg Asp Leu Ala Leu Pro Ile
1 5 10 15

Val Leu Gly Ala Leu Glu Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

Gly Val Ala Leu Ile Glu Asp Gly Lys Leu Ile Val Glu Lys Lys Lys
35 40 45

Gly Lys Ile Arg Glu Leu Val Lys Ala Leu Trp Gly Lys Asp Tyr Lys
50 55 60

Ala Lys Thr Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Lys Pro
65 70 75 80

Thr Asp Glu Asn Ala His Pro His Thr Asp Glu Lys Gly Glu Phe Ala
85 90 95

Val Val His Asn Gly Ile Ile Glu Asn Tyr Leu Glu Leu Lys Glu Glu
100 105 110

Leu Lys Lys Glu Gly Val Lys Phe Arg Ser Glu Thr Asp Thr Glu Val
115 120 125

Ile Ala His Leu Ile Ala Lys Asn Tyr Arg Gly Asp Leu Leu Glu Ala
130 135 140

Val Leu Lys Thr Val Lys Lys Leu Lys Gly Ala Phe Ala Phe Ala Val
145 150 155 160

Ile Thr Val His Glu Pro Asn Arg Leu Ile Gly Val Lys Gln Gly Ser
165 170 175

Pro Leu Ile Val Gly Leu Gly Glu Gly Glu Asn Phe Leu Ala Ser Asp
180 185 190

Ile Pro Ala Ile Leu Pro Tyr Thr Lys Lys Ile Ile Val Leu Asp Asp
195 200 205

Gly Glu Ile Ala Asp Leu Thr Pro Asp Thr Val Asn Ile Tyr Asn Phe
210 215 220

Glu Gly Glu Pro Val Ser Lys Glu Val Met Ile Thr Pro Trp Asp Leu
225 230 235 240

Val Ser Ala Glu Lys Gly Gly Phe Lys His Phe Met Leu Lys Glu Ile
245 250 255

Tyr Glu Gln Pro Lys Ala Ile Asn Asp Thr Leu Lys Gly Phe Leu Ser
260 265 270

Thr Glu Asp Ala Ile Pro Phe Lys Leu Lys Asp Phe Arg Arg Val Leu
275 280 285

Ile Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Phe Val Gly Lys Tyr
290 295 300

Trp Ile Glu Arg Phe Ala Gly Val Pro Thr Glu Val Ile Tyr Ala Ser
305 310 315 320

Glu Phe Arg Tyr Ala Asp Val Pro Val Ser Asp Lys Asp Ile Val Ile
325 330 335

Gly Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Lys Phe Ala Leu Gln
340 345 350

Ser Ala Lys Glu Lys Gly Ala Phe Thr Val Gly Leu Val Asn Val Val
355 360 365

Gly Ser Ala Ile Asp Arg Glu Ser Asp Phe Ser Leu His Thr His Ala
370 375 380

Gly Pro Glu Ile Gly Val Ala Ala Thr Lys Thr Phe Thr Ala Gln Phe
385 390 395 400

Thr Ala Leu Tyr Ala Leu Ser Val Arg Glu Ser Glu Glu Arg Glu Asn
405 410 415

Leu Ile Arg Leu Leu Glu Lys Val Pro Ser L u Val Glu Gln Thr Leu
420 425 430

Asn Thr Ala Glu Glu Val Glu Lys Val Ala Glu Lys Tyr Met Lys Lys
435 440 445

Lys Asn Met Leu Tyr Leu Gly Arg Tyr Leu Asn Tyr Pro Ile Ala Leu
450 455 460

Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Gly
465 470 475 480

Tyr Pro Ala Gly Glu Met Lys His Gly Pro Ile Ala Leu Ile Asp Glu
485 490 495

Asn Met Pro Val Val Val Ile Ala Pro Lys Asp Arg Val Tyr Glu Lys
500 505 510

Ile Leu Ser Asn Val Glu Glu Val Leu Ala Arg Lys Gly Arg Val Ile
515 520 525

Ser Val Gly Phe Lys Gly Asp Glu Thr Leu Lys Ser Lys Ser Glu Ser
530 535 540

Val Met Glu Ile Pro Lys Ala Glu Glu Pro Ile Thr Pro Phe Leu Thr
545 550 555 560

Val Ile Pro Leu Gln Leu Phe Ala Tyr Phe Ile Ala Ser Lys Leu Gly
565 570 575

Leu Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Thr Val Thr Val Glu
580 585 590

<210> 31
<211> 354
<212> PRT
<213> Aquifex

<400> 31

Met Ile Pro Gln Arg Ile Lys Glu Leu Glu Ala Tyr Lys Thr Glu Val
1 5 10 15

Thr Pro Ala Ser Val Arg Leu Ser Ser Asn Glu Phe Pro Tyr Asp Phe
20 25 30

Pro Glu Glu Ile Lys Gln Arg Ala Leu Glu Glu Leu Lys Lys Val Pro
35 40 45

Leu Asn Lys Tyr Pro Asp Pro Glu Ala Lys Glu Leu Lys Ala Val Leu
50 55 60

Ala Asp Phe Phe Gly Val Lys Glu Glu Asn Leu Val Leu Gly Asn Gly
65 70 75 80

Ser Asp Glu Leu Ile Tyr Tyr Leu Ser Ile Ala Ile Gly Glu Leu Tyr
85 90 95

Ile Pro Val Tyr Ile Pro Val Pro Thr Phe Pro Met Tyr Glu Ile Ser
100 105 110

Ala Lys Val Leu Gly Arg Pro Leu Val Lys Val Gln Leu Asp Glu Asn
115 120 125

Phe Asp Ile Asp Leu Glu Arg Ser Ile Glu Leu Ile Glu Lys Glu Lys
130 135 140

Pro Val Leu Gly Tyr Phe Ala Tyr Pro Asn Asn Pro Thr Gly Asn Leu
145 150 155 160

Phe Ser Arg Gly Lys Ile Glu Glu Ile Arg Asn Arg Gly Val Phe Cys
165 170 175

Val Ile Asp Glu Ala Tyr Tyr His Tyr Ser Gly Glu Thr Phe Leu Glu
180 185 190

Asp Ala Leu Lys Arg Glu Asp Thr Val Val Leu Arg Thr Leu Ser Lys
195 200 205

Ile Gly Met Ala Ser Leu Arg Val Gly Ile Leu Ile Gly Lys Gly Glu
210 215 220

Ile Val Ser Glu Ile Asn Lys Val Arg Leu Pro Phe Asn Val Thr Tyr
225 230 235 240

Pro Ser Gln Val Met Ala Lys Val Leu Leu Thr Glu Gly Arg Glu Phe
245 250 255

Leu Met Glu Lys Ile Gln Glu Val Val Thr Glu Arg Glu Arg Met Tyr
260 265 270

Asp Glu Met Lys Lys Ile Glu Gly Val Glu Val Phe Pro Ser Lys Ala
275 280 285

Asn Phe Leu Leu Phe Arg Thr Pro Tyr Pro Ala His Glu Val Tyr Gln
290 295 300

Glu Leu Leu Lys Arg Asp Val Leu Val Arg Asn Val Ser Tyr Met Glu
305 310 315 320

Gly Leu Gln Lys Cys Leu Arg Val Ser Val Gly Lys Pro Glu Glu Asn
325 330 335

Asn Lys Phe Leu Glu Ala Leu Glu Glu Ser Ile Lys Ser Leu Ser Ser
340 345 350

Ser Leu

<210> 32
<211> 303
<212> PRT

<213> Pyrobaculum aerophilum
<400> 32

Met Lys Pro Tyr Ala Lys Tyr Ile Trp Leu Asp Gly Arg Ile Leu Lys
1 5 10 15

Trp Glu Asp Ala Lys Ile His Val Leu Thr His Ala Leu His Tyr Gly
20 25 30

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Thr Ser Ile Phe Glu Gly Ile Arg Gly Tyr Trp Asn Gly Asp Asn Leu
        35                  40                  45

Leu Val Phe Arg Leu Glu Glu His Ile Asp Arg Met Tyr Arg Ser Ala
    50                  55                  60

Lys Ile Leu Gly Ile Asn Ile Pro Tyr Thr Arg Glu Glu Val Arg Gln
65                  70                  75                  80

Ala Val Leu Glu Thr Ile Lys Ala Asn Asn Phe Arg Glu Asp Val Tyr
                85                  90                  95

Ile Arg Pro Val Ala Phe Val Ala Ser Gln Thr Val Thr Leu Asp Ile
            100                 105                 110

Arg Asn Leu Glu Val Ser Leu Ala Val Ile Val Phe Pro Phe Gly Lys
        115                 120                 125

Tyr Leu Ser Pro Asn Gly Ile Lys Ala Thr Ile Val Ser Trp Arg Arg
    130                 135                 140

Val His Asn Thr Met Leu Pro Val Met Ala Lys Ile Gly Gly Ile Tyr
145                 150                 155                 160

Val Asn Ser Val Leu Ala Leu Val Glu Ala Arg Ser Arg Gly Phe Asp
                165                 170                 175

Glu Ala Leu Leu Met Asp Val Asn Gly Tyr Val Val Glu Gly Ser Gly
            180                 185                 190

Glu Asn Ile Phe Ile Val Arg Gly Gly Arg Leu Phe Thr Pro Pro Val
        195                 200                 205

His Glu Ser Ile Leu Glu Gly Ile Thr Arg Asp Thr Val Ile Lys Leu
    210                 215                 220

Ser Gly Asp Val Gly Leu Arg Val Glu Glu Lys Pro Ile Thr Arg Glu
225                 230                 235                 240

Glu Val Tyr Thr Ala Asp Glu Val Phe Leu Val Gly Thr Ala Ala Glu
                245                 250                 255

Ile Thr Pro Val Val Glu Val Asp Gly Arg Thr Ile Gly Thr Gly Lys
            260                 265                 270

Pro Gly Pro Ile Thr Thr Lys Ile Ala Glu Leu Tyr Ser Asn Val Val
        275                 280                 285

Arg Gly Lys Val Glu Lys Tyr Leu Asn Trp Ile Thr Pro Val Tyr
    290                 295                 300

<210>  33
<211>  52
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Primer for PCR

<400>  33
ccgagaattc attaaagagg agaaattaac tatggcagtc aaagtgcggc ct          52
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<210> 34
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for PCR

<400> 34
gaaggacctt cgaaacctat tcctaggagg c 31

<210> 35
<211> 1092
<212> DNA
<213> Ammonifex degensii

<220>
<221> misc_feature

<222> (986)..(987)
<223> n is any nucleotide

<400> 35
atggcagtca aagtgcggcc tgagctcagc caggtggaga tctaccgtcc cggcaaaccc 60

atcgaagagg taaagaagga gctggggctg gaggaggtag tcaagctggc ctccaacgag 120

aaccctctgg gaccttctcc caaggccgtg gcggcgctgg agggactgga ccactggcac 180

ctttacccag aaggctcaag ctatgagcta cggcaggcgc tgggtaagaa actggagata 240

gacccggaca gcatcatcgt gggttgcggc tcaagcgaag tcatccagat gctctctttg 300

gccctgctgg cgcccggcga cgaggtggtc atccctgtgc ctacctttcc ccgctatgag 360

cccctggcac ggctcatggg ggctaatccc gtaaaagttc ccttgaagga ctaccgcatc 420

gatgtggagg cagtggcccg agccctttcc ccccgtacca agctggtcta cctatgcaac 480

cccaacaacc ccaccgggac catcgtcacc cgggaggagg tggagtggtt cttggaaaag 540

gcgggggagg gggttctcac cgtgctggac gaggcctact gcgagtacgt gaccagcccc 600

gcctaccctg atgggctcga tttcctgcgc cggggctaca atgtggtggt gctgcgcacc 660

ttctccaaga tctacgggct ggccgggctg cgcatagggt acggtgtggc ggacagggag 720

ctggtggcgg aactgcaccg ggtgcgggag cctttcaatg tcagttccgc tgctcagata 780

gccgccctgg ccgccctgga agacgaagag ttcgtggcgc tttcgcgcca ggtcaacgaa 840

gaagggaagg tttttctcta ccgagaactg gagaggcggg ggatcgccta cgtgcccacc 900

gaggccaact tcctactctt cgatgccggt cgggacgagc aggaagtatt tcgccggatg 960

ctgcgccagg gagtgatcat ccgggncggg gtgggttatc ccacccactt aagggtgacc 1020

atcggcacct tggaacagaa ccagcgcttc ctggaagctt tggataaggc tctagagctt 1080

agggggtttt aa 1092

<210> 36
<211> 363
<212> PRT
<213> Ammonifex degensii

<220>
<221> VARIANT

<222> (329)..(330)
<223> Xaa is any Amino Acid

<400> 36

Met Ala Val Lys Val Arg Pro Glu Leu Ser Gln Val Glu Ile Tyr Arg
1 5 10 15

Pro Gly Lys Pro Ile Glu Glu Val Lys Lys Glu Leu Gly Leu Glu Glu
20 25 30

Val Val Lys Leu Ala Ser Asn Glu Asn Pro Leu Gly Pro Ser Pro Lys
35 40 45

Ala Val Ala Ala Leu Glu Gly Leu Asp His Trp His Leu Tyr Pro Glu
50 55 60

Gly Ser Ser Tyr Glu Leu Arg Gln Ala Leu Gly Lys Lys Leu Glu Ile
65 70 75 80

Asp Pro Asp Ser Ile Ile Val Gly Cys Gly Ser Ser Glu Val Ile Gln
85 90 95

Met Leu Ser Leu Ala Leu Leu Ala Pro Gly Asp Glu Val Val Ile Pro
100 105 110

Val Pro Thr Phe Pro Arg Tyr Glu Pro Leu Ala Arg Leu Met Gly Ala
115 120 125

Asn Pro Val Lys Val Pro Leu Lys Asp Tyr Arg Ile Asp Val Glu Ala
130 135 140

Val Ala Arg Ala Leu Ser Pro Arg Thr Lys Leu Val Tyr Leu Cys Asn
145 150 155 160

Pro Asn Asn Pro Thr Gly Thr Ile Val Thr Arg Glu Glu Val Glu Trp
165 170 175

Phe Leu Glu Lys Ala Gly Glu Gly Val Leu Thr Val Leu Asp Glu Ala
180 185 190

Tyr Cys Glu Tyr Val Thr Ser Pro Ala Tyr Pro Asp Gly Leu Asp Phe
195 200 205

L u Arg Arg Gly Tyr Asn Val Val Val Leu Arg Thr Phe Ser Lys Ile
210 215 220

Tyr Gly Leu Ala Gly Leu Arg Ile Gly Tyr Gly Val Ala Asp Arg Glu
225 230 235 240

Leu Val Ala Glu Leu His Arg Val Arg Glu Pro Phe Asn Val Ser Ser
245 250 255

Ala Ala Gln Ile Ala Ala Leu Ala Ala Leu Glu Asp Glu Glu Phe Val
260 265 270

Ala Leu Ser Arg Gln Val Asn Glu Glu Gly Lys Val Phe Leu Tyr Arg
275 280 285

Glu Leu Glu Arg Arg Gly Ile Ala Tyr Val Pro Thr Glu Ala Asn Phe
290 295 300

Leu Leu Phe Asp Ala Gly Arg Asp Glu Gln Glu Val Phe Arg Arg Met
305 310 315 320

Leu Arg Gln Gly Val Ile Ile Arg Xaa Gly Val Gly Tyr Pro Thr His
325 330 335

Leu Arg Val Thr Ile Gly Thr Leu Glu Gln Asn Gln Arg Phe Leu Glu
340 345 350

Ala Leu Asp Lys Ala Leu Glu Leu Arg Gly Val
355 360

<210> 37
<211> 52
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for PCR

<400> 37
ccgagaattc attaaagagg agaaattaac tatgagaaaa ggacttgcaa gt 52

<210> 38
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for PCR

<400> 38
tttcgggaac ttctctagat tcctaggagg c 31

<210> 39
<211> 1185
<212> DNA
<213> Aquifex

<400> 39
atgagaaaag gacttgcaag tagggtaagt cacctaaaac cttccccac gctgaccata 60

accgcaaaag caaaagaatt aagggctaaa ggagtggacg ttataggttt tggagcggga 120

gaacctgact tcgacacacc cgacttcata aaggaagcct gtataagggc tttaaggaa 180

ggaaagacca agtacgctcc ctccgcggga ataccagagc tcagagaagc tatagctgaa 240
aaactactga aagaaaacaa agttgagtac aaaccttcag agatagtcgt ttccgcagga 300
gcgaaaatgg ttctcttcct catattcatg gctatactgg acgaaggaga cgaggtttta 360
ctacctagcc cttactgggt aacttacccc gaacagataa ggttcttcgg aggggttccc 420
gttgaggttc ctctaaagaa agagaaagga tttcaattaa gtctggaaga tgtgaaagaa 480
aaggttacgg agagaacaaa agctatagtc ataaactctc cgaacaaccc cactggtgct 540
gtttacgaag aggaggaact taagaaaata gcggagtttt gcgtggagag gggcattttc 600
ataatttccg atgagtgcta tgagtacttc gtttacggtg atgcaaaatt tgttagccct 660
gcctcttttct cggatgaagt aaagaacata accttcacgg taaacgcctt ttcgaagagc 720
tattccatga ctggttggcg aataggttat gtagcgtgcc ccgaagagta cgcaaaagtg 780
atagcgagtc ttaacagcca gagtgtttcc aacgtcacta cctttgccca gtatggagct 840
cttgaggcct tgaaaaatcc aaagtctaaa gattttgtaa acgaaatgag aaatgctttt 900
gaaaggagaa gggatacggc tgtagaagag ctttctaaaa ttccaggtat ggatgtggta 960
aaacccgaag gtgcctttta catatttccg gacttctccg cttacgctga gaaactgggt 1020
ggtgatgtga aactctcgga gttccttctg gaaaaggcta aggttgcggt ggttcccggt 1080
tcggccttcg gagctcccgg atttttgagg ctttcttacg cccttttccga ggaaagactc 1140
gttgagggta taaggagaat aaagaaagcc cttgaagaga tctaa 1185

<210> 40
<211> 394
<212> PRT
<213> Aquifex

<400> 40

Met Arg Lys Gly Leu Ala Ser Arg Val Ser His Leu Lys Pro Ser Pro
1 5 10 15

Thr Leu Thr Ile Thr Ala Lys Ala Lys Glu Leu Arg Ala Lys Gly Val
20 25 30

Asp Val Ile Gly Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Asp
35 40 45

Phe Ile Lys Glu Ala Cys Ile Arg Ala Leu Arg Glu Gly Lys Thr Lys
50 55 60

Tyr Ala Pro Ser Ala Gly Ile Pro Glu Leu Arg Glu Ala Ile Ala Glu
65 70 75 80

Lys Leu Leu Lys Glu Asn Lys Val Glu Tyr Lys Pro Ser Glu Ile Val
85 90 95

Val Ser Ala Gly Ala Lys Met Val Leu Phe Leu Ile Phe Met Ala Ile

100 105 110

Leu Asp Glu Gly Asp Glu Val Leu Leu Pro Ser Pro Tyr Trp Val Thr
115 120 125

Tyr Pro Glu Gln Ile Arg Phe Phe Gly Gly Val Pro Val Glu Val Pro
130 135 140

Leu Lys Lys Glu Lys Gly Phe Gln Leu Ser Leu Glu Asp Val Lys Glu
145 150 155 160

Lys Val Thr Glu Arg Thr Lys Ala Ile Val Ile Asn Ser Pro Asn Asn
165 170 175

Pro Thr Gly Ala Val Tyr Glu Glu Glu Glu Leu Lys Lys Ile Ala Glu
180 185 190

Phe Cys Val Glu Arg Gly Ile Phe Ile Ile Ser Asp Glu Cys Tyr Glu
195 200 205

Tyr Phe Val Tyr Gly Asp Ala Lys Phe Val Ser Pro Ala Ser Phe Ser
210 215 220

Asp Glu Val Lys Asn Ile Thr Phe Thr Val Asn Ala Phe Ser Lys Ser
225 230 235 240

Tyr Ser Met Thr Gly Trp Arg Ile Gly Tyr Val Ala Cys Pro Glu Glu
245 250 255

Tyr Ala Lys Val Ile Ala Ser Leu Asn Ser Gln Ser Val Ser Asn Val
260 265 270

C10 Cont

Thr Thr Phe Ala Gln Tyr Gly Ala Leu Glu Ala Leu Lys Asn Pro Lys
275 280 285

Ser Lys Asp Phe Val Asn Glu Met Arg Asn Ala Phe Glu Arg Arg Arg
290 295 300

Asp Thr Ala Val Glu Glu Leu Ser Lys Ile Pro Gly Met Asp Val Val
305 310 315 320

Lys Pro Glu Gly Ala Phe Tyr Ile Phe Pro Asp Phe Ser Ala Tyr Ala
325 330 335

Glu Lys Leu Gly Gly Asp Val Lys Leu Ser Glu Phe Leu Leu Glu Lys
340 345 350

Ala Lys Val Ala Val Val Pro Gly Ser Ala Phe Gly Ala Pro Gly Phe
355 360 365

Leu Arg Leu Ser Tyr Ala Leu Ser Glu Glu Arg Leu Val Glu Gly Ile
370 375 380

Arg Arg Ile Lys Lys Ala Leu Glu Glu Ile
385 390